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SEQUENCE LISTING

<110> Igawa, Tomoyuki
Sekimori, Yasuo

<120> IgM high concentration stabilized solution

<130> 14875-159US1

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<150> JP 2003-351388

<151> 2003-10-09

<160> 18

<170> PatentIn version 3.1

<210> 1

<211> 1779

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (1)..(1779)

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gtc cag tgt gag gtg cag ctg ttg gat tct ggg gga ggc ttg gta cag 96
Val Gln Cys Glu Val Gln Leu Leu Asp Ser Gly Gly Leu Val Gln
20 25 30

cct ggg tgc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt 144
Pro Gly Gly Cys Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

agc agc tgt gcc atg agc tgg gtc cgc cag gct cca ggg aag ggg ctg 192
Ser Ser Cys Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

gag tgg gtc tca gct att agt ggt agt ggt ggt agc aca tac tac gca 240
Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Ser Thr Tyr Tyr Ala
65 70 75 80

gac tcc gtg aag ggc cgg ttc acc atc tcc aga gac aaa tcc aag aac 288
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Lys Ser Lys Asn
85 90 95

acg ttg tat ctg caa atg aac agc ctg aga gcc gag gac acg gcc gta 336
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
100 105 110

tat tac tgt gcg aaa ggt ggc aac gat att ttg act ggt tat tat gct Tyr Tyr Cys Ala Lys Gly Gly Asn Asp Ile Leu Thr Gly Tyr Tyr Ala 115 120 125	384
tgg ggc cag gga acc ctg gtc acc gtc tcc tca ggg agt gca tcc gcc Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser Ala Ser Ala 130 135 140	432
cca acc ctt ttc ccc ctc gtc tcc tgt gag aat tcc ccg tcg gat acg Pro Thr Leu Phe Pro Leu Val Ser Cys Glu Asn Ser Pro Ser Asp Thr 145 150 155 160	480
agc agc gtg gcc gtt ggc tgc ctc gca cag gac ttc ctt ccc gac tcc Ser Ser Val Ala Val Gly Cys Leu Ala Gln Asp Phe Leu Pro Asp Ser 165 170 175	528
atc act ttc tcc tgg aaa tac aag aac aac tct gac atc agc agc acc Ile Thr Phe Ser Trp Lys Tyr Lys Asn Asn Ser Asp Ile Ser Ser Thr 180 185 190	576
cgg ggc ttc cca tca gtc ctg aga ggg ggc aag tac gca gcc acc tca Arg Gly Phe Pro Ser Val Leu Arg Gly Lys Tyr Ala Ala Thr Ser 195 200 205	624
cag gtg ctg ctg cct tcc aag gac gtc atg cag ggc aca gac gaa cac Gln Val Leu Leu Pro Ser Lys Asp Val Met Gln Gly Thr Asp Glu His 210 215 220	672
gtg gtg tgc aaa gtc cag cac ccc aac ggc aac aaa gaa aag aac gtg Val Val Cys Lys Val Gln His Pro Asn Gly Asn Lys Glu Lys Asn Val 225 230 235 240	720
cct ctt cca gtg att gct gag ctg cct ccc aaa gtg agc gtc ttc gtc Pro Leu Pro Val Ile Ala Glu Leu Pro Pro Lys Val Ser Val Phe Val 245 250 255	768
cca ccc cgc gac ggc ttc ttc ggc aac ccc cgc aag tcc aag ctc atc Pro Pro Arg Asp Gly Phe Phe Gly Asn Pro Arg Lys Ser Lys Leu Ile 260 265 270	816
tgc cag gcc acg ggt ttc agt ccc cgg cag att cag gtg tcc tgg ctg Cys Gln Ala Thr Gly Phe Ser Pro Arg Gln Ile Gln Val Ser Trp Leu 275 280 285	864
cgc gag ggg aag cag gtg ggg tct ggc gtc acc acg gac cag gtg cag Arg Glu Gly Lys Gln Val Gly Ser Gly Val Thr Thr Asp Gln Val Gln 290 295 300	912
gct gag gcc aaa gag tct ggg ccc acg acc tac aag gtg acc agc aca Ala Glu Ala Lys Glu Ser Gly Pro Thr Thr Tyr Lys Val Thr Ser Thr 305 310 315 320	960
ctg acc atc aaa gag agc gac tgg ctc ggc cag agc atg ttc acc tgc Leu Thr Ile Lys Glu Ser Asp Trp Leu Gly Gln Ser Met Phe Thr Cys 325 330 335	1008

cgc gtg gat cac agg ggc ctg acc ttc cag cag aat gcg tcc tcc atg Arg Val Asp His Arg Gly Leu Thr Phe Gln Gln Asn Ala Ser Ser Met 340 345 350	1056
tgt gtc ccc gat caa gac aca gcc atc cggttgcgccatccc Cys Val Pro Asp Gln Asp Thr Ala Ile Arg Val Phe Ala Ile Pro Pro 355 360 365	1104
tcc ttt gcc agc atc ttc ctc acc aag tcc acc aag ttg acc tgc ctg Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser Thr Lys Leu Thr Cys Leu 370 375 380	1152
gtc aca gac ctg acc acc tat gac agc gtg acc atc tcc tgg acc cgc Val Thr Asp Leu Thr Tyr Asp Ser Val Thr Ile Ser Trp Thr Arg 385 390 395 400	1200
cag aat ggc gaa gct gtg aaa acc cac acc aac atc tcc gag agc cac Gln Asn Gly Glu Ala Val Lys Thr His Thr Asn Ile Ser Glu Ser His 405 410 415	1248
ccc aat gcc act ttc agc gcc gtg ggt gag gcc agc atc tgc gag gat Pro Asn Ala Thr Phe Ser Ala Val Gly Glu Ala Ser Ile Cys Glu Asp 420 425 430	1296
gac tgg aat tcc ggg gag agg ttc acg tgc acc gtg acc cac aca gac Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys Thr Val Thr His Thr Asp 435 440 445	1344
ctg ccc tcg cca ctg aag cag acc atc tcc cgg ccc aag ggg gtg gcc Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser Arg Pro Lys Gly Val Ala 450 455 460	1392
ctg cac agg ccc gat gtc tac ttg ctg cca cca gcc cgg gag cag ctg Leu His Arg Pro Asp Val Tyr Leu Leu Pro Pro Ala Arg Glu Gln Leu 465 470 475 480	1440
aac ctg cgg gag tcg gcc acc atc acg tgc ctg gtg acg ggc ttc tct Asn Leu Arg Glu Ser Ala Thr Ile Thr Cys Leu Val Thr Gly Phe Ser 485 490 495	1488
ccc gcg gac gtc ttc gtg cag tgg atg cag agg ggg cag ccc ttg tcc Pro Ala Asp Val Phe Val Gln Trp Met Gln Arg Gly Gln Pro Leu Ser 500 505 510	1536
ccg gag aag tat gtg acc agc gcc cca atg cct gag ccc cag gcc cca Pro Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu Pro Gln Ala Pro 515 520 525	1584
ggc cgg tac ttc gcc cac agc atc ctg acc gtg tcc gaa gag gaa tgg Gly Arg Tyr Phe Ala His Ser Ile Leu Thr Val Ser Glu Glu Glu Trp 530 535 540	1632
aac acg ggg gag acc tac acc tgc gtg gtg gcc cat gag gcc ctg ccc Asn Thr Gly Glu Thr Tyr Thr Cys Val Val Ala His Glu Ala Leu Pro 545 550 555 560	1680
aac agg gtc acc gag agg acc gtg gac aag tcc acc ggt aaa ccc acc	1728

Asn Arg Val Thr Glu Arg Thr Val Asp Lys Ser Thr Gly Lys Pro Thr
 565 570 575

ctg tac aac gtg tcc ctg gtc atg tcc gac aca gct ggc acc tgc tac 1776
 Leu Tyr Asn Val Ser Leu Val Met Ser Asp Thr Ala Gly Thr Cys Tyr
 580 585 590

tga 1779

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<212> PRT
<213> Homo sapiens

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20 25 30
Pro Gly Gly Cys Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45
Ser Ser Cys Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60
Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Ser Thr Tyr Tyr Ala
65 70 75 80
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Lys Ser Lys Asn
85 90 95
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
100 105 110
Tyr Tyr Cys Ala Lys Gly Gly Asn Asp Ile Leu Thr Gly Tyr Tyr Ala
115 120 125
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser Ala Ser Ala
130 135 140
Pro Thr Leu Phe Pro Leu Val Ser Cys Glu Asn Ser Pro Ser Asp Thr
145 150 155 160
Ser Ser Val Ala Val Gly Cys Leu Ala Gln Asp Phe Leu Pro Asp Ser
165 170 175
Ile Thr Phe Ser Trp Lys Tyr Lys Asn Asn Ser Asp Ile Ser Ser Thr
180 185 190
Arg Gly Phe Pro Ser Val Leu Arg Gly Gly Lys Tyr Ala Ala Thr Ser
195 200 205
Gln Val Leu Leu Pro Ser Lys Asp Val Met Gln Gly Thr Asp Glu His
210 215 220
Val Val Cys Lys Val Gln His Pro Asn Gly Asn Lys Glu Lys Asn Val
225 230 235 240
Pro Leu Pro Val Ile Ala Glu Leu Pro Pro Lys Val Ser Val Phe Val
245 250 255
Pro Pro Arg Asp Gly Phe Phe Gly Asn Pro Arg Lys Ser Lys Leu Ile
260 265 270
Cys Gln Ala Thr Gly Phe Ser Pro Arg Gln Ile Gln Val Ser Trp Leu
275 280 285
Arg Glu Gly Lys Gln Val Gly Ser Gly Val Thr Thr Asp Gln Val Gln
290 295 300
Ala Glu Ala Lys Glu Ser Gly Pro Thr Thr Tyr Lys Val Thr Ser Thr
305 310 315 320
Leu Thr Ile Lys Glu Ser Asp Trp Leu Gly Gln Ser Met Phe Thr Cys

	325	330	335
Arg Val Asp His Arg Gly Leu Thr Phe Gln Gln Asn Ala Ser Ser Met	340	345	350
Cys Val Pro Asp Gln Asp Thr Ala Ile Arg Val Phe Ala Ile Pro Pro	355	360	365
Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser Thr Lys Leu Thr Cys Leu	370	375	380
Val Thr Asp Leu Thr Thr Tyr Asp Ser Val Thr Ile Ser Trp Thr Arg	385	390	395
Gln Asn Gly Glu Ala Val Lys Thr His Thr Asn Ile Ser Glu Ser His	405	410	415
Pro Asn Ala Thr Phe Ser Ala Val Gly Glu Ala Ser Ile Cys Glu Asp	420	425	430
Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys Thr Val Thr His Thr Asp	435	440	445
Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser Arg Pro Lys Gly Val Ala	450	455	460
Leu His Arg Pro Asp Val Tyr Leu Leu Pro Pro Ala Arg Glu Gln Leu	465	470	475
Asn Leu Arg Glu Ser Ala Thr Ile Thr Cys Leu Val Thr Gly Phe Ser	485	490	495
Pro Ala Asp Val Phe Val Gln Trp Met Gln Arg Gly Gln Pro Leu Ser	500	505	510
Pro Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu Pro Gln Ala Pro	515	520	525
Gly Arg Tyr Phe Ala His Ser Ile Leu Thr Val Ser Glu Glu Glu Trp	530	535	540
Asn Thr Gly Glu Thr Tyr Thr Cys Val Val Ala His Glu Ala Leu Pro	545	550	555
Asn Arg Val Thr Glu Arg Thr Val Asp Lys Ser Thr Gly Lys Pro Thr	565	570	575
Leu Tyr Asn Val Ser Leu Val Met Ser Asp Thr Ala Gly Thr Cys Tyr	580	585	590

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1 5 10 15		
ggt gcc tac ggg gac atc gtg atg acc cag tct cca gac tcc ctg gct		96
Gly Ala Tyr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala		
20 25 30		
gtg tct ctg ggc gag agg gcc acc atc aac tgc aag tcc agc cag agt		144
Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser		
35 40 45		

gtt tta tac agc tcc aac aat aag aac tac tta gct tgg tac cag cag		192	
Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln			
50	55	60	
aaa cca gga cag cct cct aag ctg ctc att tac tgg gca tct acc cg		240	
Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg			
65	70	75	80
gaa tcc ggg gtc cct gac cga ttc agt ggc agc ggg tct ggg aca gat		288	
Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Thr Asp			
85	90	95	
ttc act ctc acc atc agc agc ctg cag gct gaa gat gtg gca gtt tat		336	
Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr			
100	105	110	
tac tgt cag caa tat tat agt act cct ccg acg ttc ggc caa ggg acc		384	
Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr			
115	120	125	
aag gtg gaa atc aaa cga act gtg gct gca cca tct gtc ttc atc ttc		432	
Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe			
130	135	140	
ccg cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc		480	
Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys			
145	150	155	160
ctg ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg		528	
Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val			
165	170	175	
gat aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag		576	
Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln			
180	185	190	
gac agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc		624	
Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Thr Leu Thr Leu Ser			
195	200	205	
aaa gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat		672	
Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His			
210	215	220	
cag ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt		720	
Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys			
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 Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser
 35 40 45
 Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln
 50 55 60
 Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
 65 70 75 80
 Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
 85 90 95
 Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr
 100 105 110
 Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr
 115 120 125
 Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe
 130 135 140
 Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys
 145 150 155 160
 Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val
 165 170 175
 Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln
 180 185 190
 Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser
 195 200 205
 Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His
 210 215 220
 Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 225 230 235 240

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<213> Homo sapiens

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 1 5 10 15

 gct gtt cat gtg aaa gcc caa gaa gat gaa agg att gtt ctt gtt gac 96
 Ala Val His Val Lys Ala Gln Glu Asp Glu Arg Ile Val Leu Val Asp
 20 25 30

 aac aaa tgt aag tgt gcc cg att act tcc agg atc atc cgt tct tcc 144
 Asn Lys Cys Lys Cys Ala Arg Ile Thr Ser Arg Ile Ile Arg Ser Ser
 35 40 45

 gaa gat cct aat gag gac att gtg gag aga aac atc cga att att gtt 192

Glu Asp Pro Asn Glu Asp Ile Val Glu Arg Asn Ile Arg Ile Ile Val			
50	55	60	
cct ctg aac aac agg gag aat atc tct gat ccc acc tca cca ttg aga			240
Pro Leu Asn Asn Arg Glu Asn Ile Ser Asp Pro Thr Ser Pro Leu Arg			
65	70	75	80
acc aga ttt gtg tac cat ttg tct gac ctc tgt aaa aaa tgt gat cct			288
Thr Arg Phe Val Tyr His Leu Ser Asp Leu Cys Lys Lys Cys Asp Pro			
85	90	95	
aca gaa gtg gag ctg gat aat cag ata gtt act gct acc cag agc aat			336
Thr Glu Val Glu Leu Asp Asn Gln Ile Val Thr Ala Thr Gln Ser Asn			
100	105	110	
atc tgt gat gaa gac agt gct aca gag acc tgc tac act tat gac aga			384
Ile Cys Asp Glu Asp Ser Ala Thr Glu Thr Cys Tyr Thr Tyr Asp Arg			
115	120	125	
aac aag tgc tac aca gct gtg gtc cca ctc gta tat ggt ggt gag acc			432
Asn Lys Cys Tyr Thr Ala Val Val Pro Leu Val Tyr Gly Gly Glu Thr			
130	135	140	
aaa atg gtg gaa aca gcc tta acc cca gat gcc tgc tat cct gac taa			480
Lys Met Val Glu Thr Ala Leu Thr Pro Asp Ala Cys Tyr Pro Asp			
145	150	155	

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<212> PRT
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Asn Lys Cys Lys Cys Ala Arg Ile Thr Ser Arg Ile Ile Arg Ser Ser			
35	40	45	
Glu Asp Pro Asn Glu Asp Ile Val Glu Arg Asn Ile Arg Ile Ile Val			
50	55	60	
Pro Leu Asn Asn Arg Glu Asn Ile Ser Asp Pro Thr Ser Pro Leu Arg			
65	70	75	80
Thr Arg Phe Val Tyr His Leu Ser Asp Leu Cys Lys Lys Cys Asp Pro			
85	90	95	
Thr Glu Val Glu Leu Asp Asn Gln Ile Val Thr Ala Thr Gln Ser Asn			
100	105	110	
Ile Cys Asp Glu Asp Ser Ala Thr Glu Thr Cys Tyr Thr Tyr Asp Arg			
115	120	125	
Asn Lys Cys Tyr Thr Ala Val Val Pro Leu Val Tyr Gly Gly Glu Thr			
130	135	140	
Lys Met Val Glu Thr Ala Leu Thr Pro Asp Ala Cys Tyr Pro Asp			
145	150	155	

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<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized sequence

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ccaacggcaa caaagaaaaag aacg 24

<210> 8
<211> 24
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<213> Artificial

<220>
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aacatgctct ggccgagcca gtcg 24

<210> 9
<211> 24
<212> DNA
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<220>
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<400> 9
gcaagtccag ccagagtgtt ttat 24

<210> 10
<211> 24
<212> DNA
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<400> 10
ctgtccttgc tgtcctgctc ttgt 24

<210> 11
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<212> DNA		
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<211> 32		
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<211> 30		
<212> DNA		
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<223> an artificially synthesized sequence		
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accattgaga accagatttg tgta		24
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24

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<211> 28
<212> DNA
<213> Artificial

<220>
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28

<210> 18
<211> 26
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized primer sequence

<400> 18
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26